

05/0
10/25

Turner

OIPE

-4-5

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/854,845

DATE: 10/24/2001

TIME: 15:00:16

Input Set : A:\LEX-0177-USA SEQLISTtxt
 Output Set: N:\CRF3\10242001\I854845.raw

3 <110> APPLICANT: Walke, D. Wade
 4 Wang, Xiaoming
 5 Scoville, John
 6 Turner, C. Alexander Jr.
 8 <120> TITLE OF INVENTION: Novel Human Semaphorin Homologs and Polynucleotides Encoding
 the Same
 10 <130> FILE REFERENCE: LEX-0177-USA
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/854,845 DK
 C--> 12 <141> CURRENT FILING DATE: 2001-05-14 DK
 12 <150> PRIOR APPLICATION NUMBER: US 60/205,274
 13 <151> PRIOR FILING DATE: 2000-05-18
 15 <150> PRIOR APPLICATION NUMBER: US 60/208,893
 16 <151> PRIOR FILING DATE: 2000-06-02
 18 <160> NUMBER OF SEQ ID NOS: 50
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3150
 24 <212> TYPE: DNA
 25 <213> ORGANISM: homo sapiens
 27 <400> SEQUENCE: 1

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30 aggaactacc tcttcagact cagccttgcc aatgtctctc ttcttcaggc cacagagtgg	180
31 gcctccagtg aggacacgctg ccgctctgc caaagcaaag ggaagactga ggaggagtgt	240
32 cagaactacg tgcgagtcct gatcgctgccc ggcggaaagg tggatgttgc tggaaaccaat	300
33 gcctttccc ccatgtcac cagcagacag gtggggaaacc tcagccggac tattgagaag	360
34 atcaatggtg tggcccctg cccctatgac ccacgccaca actccacagc tgtcatctcc	420
35 tcccagggggg agctctatgc agccacggtc atcgacttct caggtcgaaa ccctgcccc	480
36 taccgcagcc tggcagttgg gccacccgtt cgcactgccc aataataactc caagtggctt	540
37 aatgagccaa acttcgtggc agcttatgtt attggctgt ttgcataactt cttctgcgg	600
38 gagaacgcag tggagcacga ctgtggacgc accgtgtact ctcgcgtggc ccgcgtgtgc	660
39 aagaatgacg tggggggccg attcctgtgtt gaggacacat ggaccacatt catgaaggcc	720
40 cggctcaact gctccccc gggcgaggcc cccttctact ataacgagct gcagagtgc	780
41 ttccacttgc crgagcagga cctcatctat ggagtttca caaccaacgt aaacacgaty	840
42 gcggcttctg ctgtctgcgc ctcaacccctc agtgcatactt cccaggctt caatggccca	900
43 ttctcgatacc aggagaaccc cagggtgtcc tggctccca tagccaaccc catccccat	960
44 ttccagttgtg gcaccctgccc tgagaccggc cccaaacgaga acctgacggc ggcgcggctg	1020
45 caggacgcgc agcgcctctt cctgatgagc gaggccgtgc agccgggtgac acccgagccc	1080
46 tgggtcaccgc aggacagcgt ggccttctca cacctcggtt tggacctggc gcaggctaaa	1140
47 gacacgtctt accatgtactt ctacattggc accgagtcgg gcaccatctt gaaggcgctg	1200
48 tccacggcga gccgcggcctt ccacggctgc tacctggagg agctgcacgt gctggccccc	1260
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50 gggctgagag acggcgctt ggggtccca ctggagaggt ggcggcccta ccgcagccag	1380
51 ggggcattgcc tggggggccg ggaccgtac tgggtggc acgggaagca gcaacgttgc	1440
52 agcacactcg aggacagctc caacatgagc ctctggaccc agaacatcac cgcctgtctt	1500
53 gtgcggaatg tgacacggga tgggggttgc ggcctatggt caccatggc accatgttag	1560
54 cacttggatg gggacaactc aggtcttgc ctgtgtcgag ctgcgttgc tgattccct	1620
55 cgaccccgctt gtggggccct tgactgcctt gggccagcca tccacatcgcaactgttcc	1680

ENTERED

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58	tgcgtggca	agagccggga	ggaacggttc	tgtaatgaga	acacgccttg	cccggtgccc	1860
59	atcttctggg	cttctgggg	ctcctggagc	aagtgcagca	gcaactgtgg	agggggcatg	1920
60	cagtcgcggc	gtcgggctg	cgagaacggc	aactcctgcc	tgggctgccc	cgtggagttc	1980
61	aagacgtgca	accccgaggg	ctgccccgaa	gtgcggcgca	acacccctg	gacgccgtgg	2040
62	ctgcccgtga	acgtgacgca	ggcgggggca	cggcaggagc	agcggttccg	tttcacactgc	2100
63	cgcgcgcggc	ttgcagaccc	gcacggctg	cagttcgca	ggagaaggac	cgagacgagg	2160
64	acctgtcccg	cgacggctc	cgctcctgc	gacaccgacg	ccctggtgga	ggacccctcg	2220
65	cgcagcggga	gcacccccc	gcacacggtg	agcgggggt	gggcccctg	gggcccgtgg	2280
66	tgcgtctgtct	cccgggactg	cgagctgggc	ttccgcgtcc	gcaagagaac	gtgcactaac	2340
67	ccggagccccc	gcaacggggg	cctgcctgc	gtggcgatg	ctgcccggata	ccaggactgc	2400
68	aaccccccagg	cttgcctcagt	tgggggtgct	tggtcctgct	ggacccatg	gtctccatgc	2460
69	tcaagttccct	gtgggtgggg	tcaactatcaa	cgcacccgtt	cctgcaccag	ccccgcaccc	2520
70	tcccccagggt	aggacatctg	tctcgggtc	cacacggagg	aggcactatg	tgcacacacag	2580
71	gcctgcccag	aaggctggc	gccctggtct	gagtggagta	agtgcactga	cgacggagcc	2640
72	cagagccgaa	gccggcactg	tgaggagctc	ctcccaagggt	ccagccctg	tgctggaaac	2700
73	agoagccaga	gcccccctg	cccttacagc	gagattcccg	tcatcctgcc	agcctccagc	2760
74	atggaggagg	ccaccggctg	tgagggttc	aatctcatcc	acttggtgcc	cacgggcac	2820
75	tcctgcttct	tgggctctgg	gctcctgacc	ctagcagtgt	acctgtctg	ccagcactgc	2880
76	cagcgtcagt	cccaggagtc	cacactggtc	catcctgcca	cccccaacca	tttgactac	2940
77	aaggcggag	gcaccccgaa	gaatgaaaag	tacacaccca	tgaaattcaa	gaccctgaac	3000
78	aagaataact	tgatccctga	tgacagagcc	aacttctacc	cattgcagca	gaccaatgtg	3060
79	tacacgacta	cttactaccc	aagcccccctg	aacaaacaca	gcttccggcc	cgaggcctca	3120
80	cctggacaac	ggtgctccc	caacagctga				3150

82 <210> SEQ ID NO: 2

83 <211> LENGTH: 1049

84 <212> TYPE: PRT

85 <213> ORGANISM: homo sapiens

87 <400> SEQUENCE: 2

88	Met	Thr	Val	Val	Asn	Pro	Gln	Asp	Leu	Gln	Pro	Trp	Val	Ser	Asn	Phe
89	1				5				10			15				
90	Thr	Tyr	Pro	Gly	Ala	Arg	Asp	Phe	Ser	Gln	Leu	Ala	Leu	Asp	Pro	Ser
91					20				25			30				
92	Gly	Asn	Gln	Leu	Ile	Val	Gly	Ala	Arg	Asn	Tyr	Leu	Phe	Arg	Leu	Ser
93					35				40			45				
94	Leu	Ala	Asn	Val	Ser	Leu	Leu	Gln	Ala	Thr	Glu	Trp	Ala	Ser	Ser	Glu
95					50				55			60				
96	Asp	Thr	Arg	Arg	Ser	Cys	Gln	Ser	Lys	Gly	Lys	Thr	Glu	Glu	Glu	Cys
97	65				70				75			80				
98	Gln	Asn	Tyr	Val	Arg	Val	Leu	Ile	Val	Ala	Gly	Arg	Lys	Val	Phe	Met
99					85				90			95				
100	Cys	Gly	Thr	Asn	Ala	Phe	Ser	Pro	Met	Cys	Thr	Ser	Arg	Gln	Val	Gly
101					100				105			110				
102	Asn	Leu	Ser	Arg	Thr	Ile	Glu	Lys	Ile	Asn	Gly	Val	Ala	Arg	Cys	Pro
103					115				120			125				
104	Tyr	Asp	Pro	Arg	His	Asn	Ser	Thr	Ala	Val	Ile	Ser	Ser	Gln	Gly	Glu
105					130				135			140				
106	Leu	Tyr	Ala	Ala	Thr	Val	Ile	Asp	Phe	Ser	Gly	Arg	Asp	Pro	Ala	Ile

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107	145	150	155	160
108	Tyr Arg Ser Leu Gly Ser Gly Pro Pro Leu Arg Thr Ala Gln Tyr Asn			
109	165	170	175	
110	Ser Lys Trp Leu Asn Glu Pro Asn Phe Val Ala Ala Tyr Asp Ile Gly			
111	180	185	190	
112	Leu Phe Ala Tyr Phe Phe Leu Arg Glu Asn Ala Val Glu His Asp Cys			
113	195	200	205	
114	Gly Arg Thr Val Tyr Ser Arg Val Ala Arg Val Cys Lys Asn Asp Val			
115	210	215	220	
116	Gly Gly Arg Phe Leu Leu Glu Asp Thr Trp Thr Thr Phe Met Lys Ala			
117	225	230	235	240
118	Arg Leu Asn Cys Ser Arg Pro Gly Glu Val Pro Phe Tyr Tyr Asn Glu			
119	245	250	255	
120	Leu Gln Ser Ala Phe His Leu Pro Glu Gln Asp Leu Ile Tyr Gly Val			
121	260	265	270	
122	Phe Thr Thr Asn Val Asn Ser Ile Ala Ala Ser Ala Val Cys Ala Phe			
123	275	280	285	
124	Asn Leu Ser Ala Ile Ser Gln Ala Phe Asn Gly Pro Phe Arg Tyr Gln			
125	290	295	300	
126	Glu Asn Pro Arg Ala Ala Trp Leu Pro Ile Ala Asn Pro Ile Pro Asn			
127	305	310	315	320
128	Phe Gln Cys Gly Thr Leu Pro Glu Thr Gly Pro Asn Glu Asn Leu Thr			
129	325	330	335	
130	Glu Arg Ser Leu Gln Asp Ala Gln Arg Leu Phe Leu Met Ser Glu Ala			
131	340	345	350	
132	Val Gln Pro Val Thr Pro Glu Pro Cys Val Thr Gln Asp Ser Val Arg			
133	355	360	365	
134	Phe Ser His Leu Val Val Asp Leu Val Gln Ala Lys Asp Thr Leu Tyr			
135	370	375	380	
136	His Val Leu Tyr Ile Gly Thr Glu Ser Gly Thr Ile Leu Lys Ala Leu			
137	385	390	395	400
138	Ser Thr Ala Ser Arg Ser Leu His Gly Cys Tyr Leu Glu Glu Leu His			
139	405	410	415	
140	Val Leu Pro Pro Gly Arg Arg Glu Pro Leu Arg Ser Leu Arg Ile Leu			
141	420	425	430	
142	His Ser Ala Arg Ala Leu Phe Val Gly Leu Arg Asp Gly Val Leu Arg			
143	435	440	445	
144	Val Pro Leu Glu Arg Cys Ala Ala Tyr Arg Ser Gln Gly Ala Cys Leu			
145	450	455	460	
146	Gly Ala Arg Asp Pro Tyr Cys Gly Trp Asp Gly Lys Gln Gln Arg Cys			
147	465	470	475	480
148	Ser Thr Leu Glu Asp Ser Ser Asn Met Ser Leu Trp Thr Gln Asn Ile			
149	485	490	495	
150	Thr Ala Cys Pro Val Arg Asn Val Thr Arg Asp Gly Gly Phe Gly Pro			
151	500	505	510	
152	Trp Ser Pro Trp Gln Pro Cys Glu His Leu Asp Gly Asp Asn Ser Gly			
153	515	520	525	
154	Ser Cys Leu Cys Arg Ala Arg Ser Cys Asp Ser Pro Arg Pro Arg Cys			
155	530	535	540	

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156 Gly Gly Leu Asp Cys Leu Gly Pro Ala Ile His Ile Ala Asn Cys Ser
157 545 550 555 560
158 Arg Asn Gly Ala Trp Thr Pro Trp Ser Ser Trp Ala Leu Cys Ser Thr
159 565 570 575
160 Ser Cys Gly Ile Gly Phe Gln Val Arg Gln Arg Ser Cys Ser Asn Pro
161 580 585 590
162 Ala Pro Arg His Gly Gly Arg Ile Cys Val Gly Lys Ser Arg Glu Glu
163 595 600 605
164 Arg Phe Cys Asn Glu Asn Thr Pro Cys Pro Val Pro Ile Phe Trp Ala
165 610 615 620
166 Ser Trp Gly Ser Trp Ser Lys Cys Ser Ser Asn Cys Gly Gly Gly Met
167 625 630 635 640
168 Gln Ser Arg Arg Arg Ala Cys Glu Asn Gly Asn Ser Cys Leu Gly Cys
169 645 650 655
170 Gly Val Glu Phe Lys Thr Cys Asn Pro Glu Gly Cys Pro Glu Val Arg
171 660 665 670
172 Arg Asn Thr Pro Trp Thr Pro Trp Leu Pro Val Asn Val Thr Gln Gly
173 675 680 685
174 Gly Ala Arg Gln Glu Gln Arg Phe Arg Phe Thr Cys Arg Ala Pro Leu
175 690 695 700
176 Ala Asp Pro His Gly Leu Gln Phe Gly Arg Arg Arg Thr Glu Thr Arg
177 705 710 715 720
178 Thr Cys Pro Ala Asp Gly Ser Gly Ser Cys Asp Thr Asp Ala Leu Val
179 725 730 735
180 Glu Asp Leu Leu Arg Ser Gly Ser Thr Ser Pro His Thr Val Ser Gly
181 740 745 750
182 Gly Trp Ala Ala Trp Gly Pro Trp Ser Ser Cys Ser Arg Asp Cys Glu
183 755 760 765
184 Leu Gly Phe Arg Val Arg Lys Arg Thr Cys Thr Asn Pro Glu Pro Arg
185 770 775 780
186 Asn Gly Gly Leu Pro Cys Val Gly Asp Ala Ala Glu Tyr Gln Asp Cys
187 785 790 795 800
188 Asn Pro Gln Ala Cys Pro Val Arg Gly Ala Trp Ser Cys Trp Thr Ser
189 805 810 815
190 Trp Ser Pro Cys Ser Ala Ser Cys Gly Gly His Tyr Gln Arg Thr
191 820 825 830
192 Arg Ser Cys Thr Ser Pro Ala Pro Ser Pro Gly Glu Asp Ile Cys Leu
193 835 840 845
194 Gly Leu His Thr Glu Glu Ala Leu Cys Ala Thr Gln Ala Cys Pro Glu
195 850 855 860
196 Gly Trp Ser Pro Trp Ser Glu Trp Ser Lys Cys Thr Asp Asp Gly Ala
197 865 870 875 880
198 Gln Ser Arg Ser Arg His Cys Glu Glu Leu Leu Pro Gly Ser Ser Ala
199 885 890 895
200 Cys Ala Gly Asn Ser Ser Gln Ser Arg Pro Cys Pro Tyr Ser Glu Ile
201 900 905 910
202 Pro Val Ile Leu Pro Ala Ser Ser Met Glu Glu Ala Thr Gly Cys Ala
203 915 920 925
204 Gly Phe Asn Leu Ile His Leu Val Ala Thr Gly Ile Ser Cys Phe Leu

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205	930	935	940	
206	Gly Ser Gly Leu Leu Thr Leu Ala Val Tyr Leu Ser Cys Gln His Cys			
207	945	950	955	960
208	Gln Arg Gln Ser Gln Glu Ser Thr Leu Val His Pro Ala Thr Pro Asn			
209	965	970	975	
210	His Leu His Tyr Lys Gly Gly Thr Pro Lys Asn Glu Lys Tyr Thr			
211	980	985	990	
212	Pro Met Glu Phe Lys Thr Leu Asn Lys Asn Asn Leu Ile Pro Asp Asp			
213	995	1000	1005	
214	Arg Ala Asn Phe Tyr Pro Leu Gln Gln Thr Asn Val Tyr Thr Thr Thr			
215	1010	1015	1020	
216	Tyr Tyr Pro Ser Pro Leu Asn Lys His Ser Phe Arg Pro Glu Ala Ser			
217	1025	1030	1035	1040
218	Pro Gly Gln Arg Cys Phe Pro Asn Ser			
219	1045			
221	<210> SEQ ID NO: 3			
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223	<212> TYPE: DNA			
224	<213> ORGANISM: homo sapiens			
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229	gcccttagca agcacccac cgtggccttt gaagacactgc agccgtgggt ctctaacttc	180		
230	acctaccctg gagccggga tttctcccaag ctggcttgg acccctccgg graccagctc	240		
231	atcggtggag ccaggaacta cctttcaga cttagccttg ccaatgtctc tcttcttcag	300		
232	gcccacagat gggctccag tgaggacacg cgccgctctt gccaaagcaa aggaagact	360		
233	gaggaggagt gtcagaacta cgtgcgagtc ctgatcgatgc cggccggaa ggttcatg	420		
234	tgtggaccca atgcctttc cccatgtgc accagcagac aggtggggaa ctcagccgg	480		
235	actattgaga agatcaatgg tgtggcccg tggccctatg acccacgcca caactccaca	540		
236	gtgtcatct cttcccgagg ggagcttat gcagccacgg tcatcgactt ctcaggctgg	600		
237	gaccctgcca tctaccgcag cctggcagt gggccaccgc ttgcactgc ccaataataac	660		
238	tccaaatggc ttaatgagcc aaacttcgtg gcagcctatg atattggct gttgcatac	720		
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242	ctgcagatgt cttcccaact gcrsgagcag gacccatct atggagttt cacaaccaac	960		
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254	accgcctgtc ctgtgcggaa tgtgcacacgg gatgggggct tcggccatgt gtcaccatgg	1680		
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date